

Table S1. Identified phenotypes.

Locus name <sup>a</sup>	NTML name	Gene symbol	Putative identification	Hemolysis <sup>b</sup>	Protease <sup>b</sup>	Pigment <sup>b</sup>	Mannitol
SAUSA300_0014	NE1942		hypothetical protein	+			
SAUSA300_0017	NE529	<i>purA</i>	adenylosuccinate synthetase			-	
SAUSA300_0157	NE1021	<i>cap5F</i>	capsular polysaccharide biosynthesis protein Cap5F	-			
SAUSA300_0188	NE945	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	-			
SAUSA300_0215	NE289		conserved hypothetical protein	-			
SAUSA300_0284	NE604		conserved hypothetical protein	-			
SAUSA300_0306	NE605	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	-	+		
SAUSA300_0322	NE1199		Oye family NADH-dependent flavin oxidoreductase	-			
SAUSA300_0355	NE1901		acetyl-CoA acetyltransferase		-		
SAUSA300_0364	NE350	<i>ychF</i>	GTP-binding protein YchF		-		
SAUSA300_0432	NE231		sodium dependent transporter		-		
SAUSA300_0462	NE396		conserved hypothetical protein		-		
SAUSA300_0473	NE1237	<i>purR</i>	pur operon repressor		-		
SAUSA300_0474	NE404		putative endoribonuclease L-PSP		-		
SAUSA300_0489	NE1313		putative cell division protein FtsH		-		
SAUSA300_0521	NE1922	<i>nusG</i>	transcription antitermination protein			-	
SAUSA300_0539	NE292	<i>ilvE</i>	branched-chain amino acid aminotransferase		+		
SAUSA300_0543	NE802		putative deaminase		-		
SAUSA300_0595	NE220		conserved hypothetical protein		-		
SAUSA300_0603	NE1358		conserved hypothetical protein	-			
SAUSA300_0605	NE1193	<i>sarA</i>	accessory regulator A		+	-	
SAUSA300_0620	NE68		ABC transporter ATP-binding protein		-		
SAUSA300_0626	NE1374		teichoic acid biosynthesis protein B	-			
SAUSA300_0630	NE1509		ABC transporter ATP-binding protein		-		
SAUSA300_0690	NE1296	<i>saeS</i>	sensor histidine kinase SaeS	-			
SAUSA300_0691	NE1622	<i>saeR</i>	DNA-binding response regulator SaeR	-	-		
SAUSA300_0752	NE912	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit		-	-	
SAUSA300_0764	NE501	<i>rnr</i>	ribonuclease R		-		
SAUSA300_0785	NE1016		acetyltransferase			-	
SAUSA300_0844	NE1884		hypothetical protein	-			
SAUSA300_0846	NE967		Na+/H+ antiporter family protein		-		
SAUSA300_0847	NE235		conserved hypothetical protein	-			
SAUSA300_0903	NE896		hypothetical protein		-	-	
SAUSA300_0904	NE1800		hypothetical protein		-	-	
SAUSA300_0905	NE1299		hypothetical protein			-	
SAUSA300_0918	NE1663		diacylglycerol glucosyltransferase	-			
SAUSA300_0947	NE28		hydrolase, alpha/beta hydrolase fold family	-	-		
SAUSA300_0961	NE1543	<i>qoxC</i>	quinol oxidase, subunit III	-	-	-	
SAUSA300_0962	NE732	<i>qoxB</i>	quinol oxidase, subunit I	-	-	-	

SAUSA300_0963	NE92	<i>qoxA</i>	quinol oxidase, subunit II		-		
SAUSA300_0984	NE1023	<i>ptsI</i>	phosphoenolpyruvate-protein phosphotransferase				-
SAUSA300_0996	NE1610	<i>lpdA</i>	dihydrolipoamide dehydrogenase	-			
SAUSA300_1002	NE658	<i>potD</i>	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein		-		
SAUSA300_1016	NE1434	<i>cyoE</i>	protoheme IX farnesyltransferase	-	-		
SAUSA300_1017	NE1084		hypothetical protein		-		
SAUSA300_1019	NE456		conserved hypothetical protein		-		
SAUSA300_1058	NE1354		alpha-hemolysin precursor	-			
SAUSA300_1092	NE1048	<i>pyrP</i>	uracil permease	-	-		
SAUSA300_1113	NE217	<i>pknB</i>	protein kinase	-			
SAUSA300_1118	NE1735		hypothetical protein	-			
SAUSA300_1119	NE229		conserved hypothetical protein	-			
SAUSA300_1127	NE1342	<i>smc</i>	chromosome segregation protein SMC			-	
SAUSA300_1138	NE569	<i>sucC</i>	succinyl-CoA synthetase, beta subunit	-	-		
SAUSA300_1145	NE883	<i>xerC</i>	tyrosine recombinase xerC		+	-	
SAUSA300_1147	NE1708	<i>hsfU</i>	ATP-dependent protease ATP-binding subunit HsfU		+		
SAUSA300_1148	NE1555	<i>codY</i>	transcriptional repressor CodY	+	+		
SAUSA300_1167	NE259	<i>pnpA</i>	polyribopolyribonucleotide nucleotidyltransferase		-		
SAUSA300_1185	NE1662	<i>miaB</i>	(dimethylallyl)adenosine tRNA methylthiotransferase		-		
SAUSA300_1255	NE1360	<i>fmtC</i>	oxacillin resistance-related FmtC protein	-			
SAUSA300_1318	NE403		DegV family protein	-			
SAUSA300_1359	NE1920		polyprenyl synthetase			+	
SAUSA300_1465	NE1829		2-oxoisovalerate dehydrogenase, E1 component, beta subunit			-	
SAUSA300_1467	NE1896	<i>lpdA</i>	dihydrolipoamide dehydrogenase			-	
SAUSA300_1469	NE1895	<i>argR</i>	arginine repressor	-		-	
SAUSA300_1470	NE1447		geranyltransterase	-		-	
SAUSA300_1472	NE458	<i>xseA</i>	exodeoxyribonuclease VII, large subunit			-	
SAUSA300_1473	NE1887	<i>nusB</i>	transcription antitermination protein NusB		-	-	
SAUSA300_1514	NE723	<i>fur</i>	ferric uptake regulation protein		-		
SAUSA300_1544	NE865	<i>lepA</i>	GTP-binding protein LepA	-			
SAUSA300_1555	NE1943	<i>aroE</i>	shikimate 5-dehydrogenase		-		
SAUSA300_1558	NE714	<i>mtnN</i>	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	-			
SAUSA300_1573	NE1794		Holliday junction resolvase-like protein			-	
SAUSA300_1615	NE1845	<i>hemB</i>	delta-aminolevulinic acid dehydratase	-			
SAUSA300_1633	NE1343	<i>gap</i>	glyceraldehyde 3-phosphate dehydrogenase 2	-		-	
SAUSA300_1644	NE1407	<i>pyk</i>	pyruvate kinase				-
SAUSA300_1648	NE525		putative NADP-dependent malic enzyme	-			
SAUSA300_1650	NE1208		hypothetical protein	-			
SAUSA300_1720	NE1909		hypothetical protein	-			
SAUSA300_1784	NE294		signal transduction protein TRAP	-			
SAUSA300_1797	NE1445		conserved hypothetical protein		-		

SAUSA300_1855	NE596	<i>sgtB</i>	monofunctional glycosyltransferase		-		
SAUSA300_1889	NE522	<i>purB</i>	adenylosuccinate lyase			-	
SAUSA300_1890	NE1278		staphopain A		-		
SAUSA300_1911	NE1908		ABC transporter ATP-binding protein	-	-	-	
SAUSA300_1912	NE1188		putative membrane protein	-			
SAUSA300_1935	NE1336		phi77 ORF029-like protein			-	
SAUSA300_1976	NE1222		succinyl-diaminopimelate desuccinylase	-			
SAUSA300_1984	NE1262		hypothetical protein	-	-		
SAUSA300_1989	NE95	<i>agrB</i>	accessory gene regulator protein B	-	-	-	
SAUSA300_1991	NE873	<i>agrC</i>	accessory gene regulator protein C	-	-	-	
SAUSA300_1992	NE1532	<i>agrA</i>	accessory gene regulator protein A	-	-	-	
SAUSA300_2022	NE1109	<i>rpoF</i>	RNA polymerase sigma factor SigB	+	+	-	
SAUSA300_2023	NE1472	<i>rsbW</i>	anti-sigma-B factor, serine-protein kinase	+	+	-	
SAUSA300_2024	NE1872	<i>rsbV</i>	anti-sigma-B factor, antagonist	+	+	-	
SAUSA300_2025	NE1607	<i>rsbU</i>	sigma-B regulation protein	+	+	-	
SAUSA300_2026	NE1833		PemK family protein	+	+	-	
SAUSA300_2027	NE1713	<i>alr</i>	alanine racemase	-			
SAUSA300_2040	NE1598		hypothetical protein	-	-		
SAUSA300_2055	NE1495	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	-			
SAUSA300_2059	NE1850	<i>atpG</i>	F0F1 ATP synthase subunit gamma	-			
SAUSA300_2060	NE592	<i>atpA</i>	ATP synthase F1, alpha subunit	-			
SAUSA300_2061	NE1889	<i>atpH</i>	F0F1 ATP synthase subunit delta	-			
SAUSA300_2064	NE1548	<i>atpB</i>	F0F1 ATP synthase subunit A	-			
SAUSA300_2071	NE997		HemK family modification methylase	-	-		
SAUSA300_2073	NE277	<i>tdk</i>	thymidine kinase	-			
SAUSA300_2075	NE149	<i>rho</i>	transcription termination factor Rho		-		
SAUSA300_2079	NE476	<i>fba</i>	fructose bisphosphate aldolase	-			
SAUSA300_2105	NE929	<i>mtlF</i>	PTS system, mannitol specific IIBC component				-
SAUSA300_2106	NE837		putative transcriptional regulator				-
SAUSA300_2107	NE1737	<i>mtlA</i>	PTS system, mannitol specific IIA component				-
SAUSA300_2108	NE1263	<i>mtlD</i>	mannitol-1-phosphate 5-dehydrogenase				-
SAUSA300_2153	NE894	<i>lacC</i>	tagatose-6-phosphate kinase		+		
SAUSA300_2156	NE436		lactose phosphotransferase system repressor		-		
SAUSA300_2174	NE829		cobalt transport family protein		-		
SAUSA300_2223	NE693	<i>mobB</i>	molybdopterin-guanine dinucleotide biosynthesis protein B	-	+	-	
SAUSA300_2224	NE603	<i>moeA</i>	molybdopterin biosynthesis protein A	-			
SAUSA300_2242	NE43	<i>ureF</i>	urease accessory protein UreF	-			
SAUSA300_2282	NE1099		hypothetical protein	-			
SAUSA300_2296	NE1933		esterase-like protein	-			
SAUSA300_2326	NE1304		transcription regulatory protein	-			
SAUSA300_2331	NE567		transcriptional regulator, MarR family		-		
SAUSA300_2365	NE1399	<i>hlgA</i>	gamma-hemolysin component A	-			

SAUSA300_2455	NE542		putative fructose-1,6-bisphosphatase		-	-	
SAUSA300_2467	NE1787	<i>srtA</i>	sortase	-			
SAUSA300_2498	NE382	<i>crtN</i>	squalene synthase			-	
SAUSA300_2499	NE1444	<i>crtM</i>	squalene desaturase			-	
SAUSA300_2500	NE518		glycosyl transferase			-	
SAUSA300_2501	NE468		phytoene dehydrogenase			-	
SAUSA300_2502	NE1538		hypothetical protein			-	
SAUSA300_2546	NE1196	<i>betB</i>	glycine betaine aldehyde dehydrogenase	-			
SAUSA300_2548	NE1690		hypothetical protein	-			
SAUSA300_2550	NE1205	<i>nrdG</i>	anaerobic ribonucleotide reductase, small subunit		-		
SAUSA300_2572	NE163	<i>aur</i>	zinc metalloproteinase aureolysin		-		
SAUSA300_2614	NE1153		hypothetical protein	-			

<sup>a</sup>Accession Number, gene name, and gene description based off of the FPR3757 genome database

<sup>b</sup>Phenotypes are designated as lower (-) or higher (+) regardless of the magnitude of the change